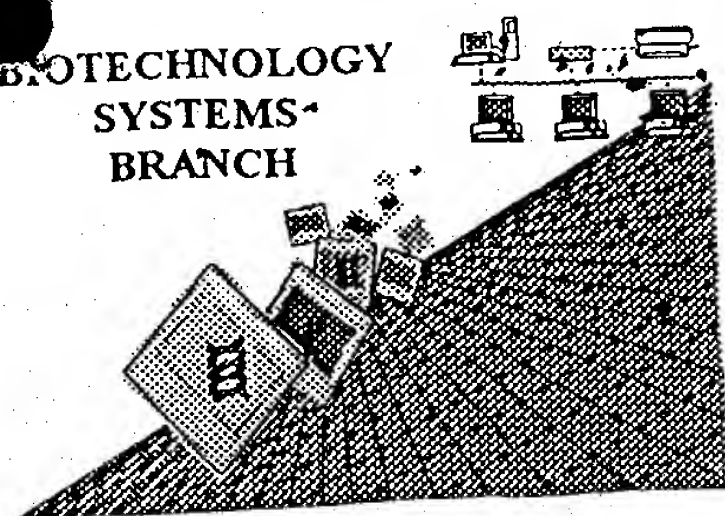


1979

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0570
0920

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 823 887A
Source: O I P E
Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/823 8877A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

See Annotations in Sequence Listing
Contact Mark Spencer at 203 308 4212

OIFE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,887A

DATE: 10/04/2001

TIME: 11:25:40

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I823887A.raw

5 <110> APPLICANT: Sanjay Kumar, Lakhvir Lal, Paramvir Singh Ahuja
 7 <120> TITLE OF INVENTION: CLONING OF NOVEL GENE SEQUENCES EXPRESSED AND REPRESSED
 DURING
 8 WINTER DORMANCY IN THE APICAL BUDS OF TEA (CAMELLIA SINENSIS L.
 9 (O.) KUNTZE) BUSH
 11 <130> FILE REFERENCE: H053916.0001US0
 W--> 12 <140> CURRENT APPLICATION NUMBER: 09/823,887A
 C--> 14 <141> CURRENT FILING DATE: 2001-09-15
 W--> 16 <150> PRIOR APPLICATION NUMBER:
 W--> 17 <151> PRIOR FILING DATE:
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE:

Does Not Comply
 Corrected Diskette Needed

See page 2 of 4 B

ERRORED SEQUENCES

23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 305
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Camellia sinensis L. (O.) Kuntze
 28 <220> FEATURE:
 W--> 29 <221> NAME/KEY: 5' clip
 30 <222> LOCATION: 31.2
 E--> 33 <400> SEQUENCE: 5
 E--> 34 atcgccgtaa ttgccatggt ttccctctca ccggaatcct acgttatcc ccttaccttc gtgaacatta
 E--> 35 cagtaggaat cgggtgtcca attatcaact taattttggg cgcattctgtt cgtgttaact agaagccatg
 E--> 36 tatacatata atacaacatg gttcactcct cctacagatt atgagttgaa cttttataat aagttgtaat
 E--> 37 aatggcttct gaataaggag aagaggagcc tctgtttggt ttacttatta cagatgtgat atcggtcaac
 E--> 38 aactttgatt ctgcgaaaa aaaaa-3
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 297
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Camellia sinensis L. (O.) Kuntze
 45 <220> FEATURE:
 W--> 46 <221> NAME/KEY: 5' clip
 47 <222> LOCATION: 21.2
 E--> 49 <400> SEQUENCE: 5
 E--> 50 agaagtacct gaaaggaagc ttaacgaggt gaacatccat tgcagccagc cctggaatct gtacagggca
 E--> 51 actctgaacc ggaattattt taataaccg tgggcaatga ttgcaattat ggctcgtttg gtattacttc
 E--> 52 tactcaacta gacacaactg tatttacggt ttctcgtgga attgtaattg ttggagcgac aaaatagatg
 E--> 53 gtcacaactt attggtgaga gtatcagtgt gctcttcttt atcgtcttta actctccgtg gtaattactt
 E--> 54 tgacaatatt catacat-3
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 239
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Camellia sinensis L. (O.) Kuntze
 61 <220> FEATURE:
 W--> 62 <221> NAME/KEY: 5' clip

Integer in sequence fields 210 and 400 must be the same.

sequence numbering inputs are required

3 character designation is invalid in the sequence listing

integer in fields 210 and 400 must be the same

Delete end of file 3 character nonnucleotide character.

Call Mark Spencer at the Biotech/Systems Division "Help Desk" 703 308 4212

60
120
180
240

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,887A

DATE: 10/04/2001

TIME: 11:25:40

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I823887A.raw

63 <222> LOCATION: 53.1 — Integer in fields 210 and 400 must match

E--> 65 <400> SEQUENCE: 5' —

E--> 66 gagactcagc tcagcaatca tgttctaagt gaatgtcact ctatgcctt cttgtccctc ttagacatac

E--> 67 tacatcctca ttctgctaga aatgaactca tgtaggtttt gaagttggga acttttgaaa ctgtgttgtt

E--> 68 tgggtgctgt ctgttatata attctctcaa ctgcggagaa ttgacgttgg ttgtagtgga attcaacact

E--> 69 tgggttttgt tcttagttaa aaaaaaaaa-3' — Delete non nucleotide characters

71 <210> SEQ ID NO: 4

72 <211> LENGTH: 228

73 <212> TYPE: DNA

74 <213> ORGANISM: Camellia sinensis L. (O.) Kuntze

76 <220> FEATURE: — Integer in fields 210 and 400 must match.

W--> 77 <221> NAME/KEY: 5' clip

78 <222> LOCATION: 44.3

E--> 80 <400> SEQUENCE: 5' —

E--> 81 atagcttagt cacgtgtctc ttgagaatgg actacgtagt tgttaagttg ggtgatcaga aggcgttgat

E--> 82 gatgaatgta tgaagcagag actactgaat gtaattttgt tgttgaaaga tgaatgattt attaatgcct

E--> 83 gcatactttt ctattgtttg atgccaaacc tttgggcaca ttttttcttt ctttttgtga taatgttctc

E--> 84 ttcttgcaaa aaaaaaaaa-3' — Delete end of sequence nonnucleotide characters

<160>

4

<170>

<210>

<211>

<212>

<213>

<220>

<221>

<222>

<400>

ATCGCCGTAA

GTGAACATTA

CGTGTTAACT

ATGAGTTGAA

TCTGTTTGTT

AAAAA-3'

1

305

DNA

Camellia sinensis L. (O.) Kuntze

5' clip

31.2

5'

TTGCCATGTT

CAGTAGGAAT

AGAAGCCATG

CTTTTATAAT

TTACTTATTA

TTCCCTCTCA

CGGTGGTCCA

TATACATACA

AAGTTGTAAT

CAGATGTGAT

CCGGAATCCT

ATTATCAACT

ATACAACATG

AATGGCTTCT

ATCGTTCAAC

ACGTTATCC

TAATTTTGGG

GTTCACTCCT

GAATAAGGAG

AACTTTGATT

CCTTACCTTC

CGCATCTGTT

CCTACAGATT

AAGAGGAGCC

CTGCGAAAAA

Label 210 and 400 must contain
the same integer

Sequence Numbering Inputs
are missing

60

120

180

240

300

305

These are
Actual File Contents as of 10/23/01

MMA

Delete 3 character
non nucleotide base designation

These types of errors exist throughout the sequence listing

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/823,887A

DATE: 10/04/2001

TIME: 11:25:41

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I823887A.raw

L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:5
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:69 SEQ:1
L:34 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=1
M:112 Repeated in SeqNo=1
L:38 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:38 M:252 E: No. of Seq. differs, <211>LENGTH:Input:305 Found:306 SEQ:1
L:46 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:49 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:5
L:50 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:70 SEQ:2
M:112 Repeated in SeqNo=2
M:254 Repeated in SeqNo=2
L:54 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:54 M:252 E: No. of Seq. differs, <211>LENGTH:Input:297 Found:299 SEQ:2
L:62 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:65 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:5
L:66 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:70 SEQ:3
M:112 Repeated in SeqNo=3
M:254 Repeated in SeqNo=3
L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:69 M:252 E: No. of Seq. differs, <211>LENGTH:Input:239 Found:241 SEQ:3
L:77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:80 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:5
L:81 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:70 SEQ:4
M:112 Repeated in SeqNo=4
M:254 Repeated in SeqNo=4
L:84 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:84 M:252 E: No. of Seq. differs, <211>LENGTH:Input:228 Found:230 SEQ:4